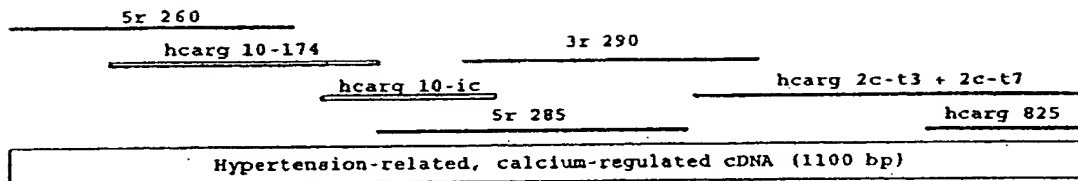


A



B

-131

GTAAAGGCTTGGTTTGTATTTGTAATCAACTGTGGTTAGGACCTTCTCTCGGACTGGTCAAGAAACGGGAAGAAAGG -80

ATG TCT GCT TTG GGG GCT GCA GCT CCA TAC TTG CAC CAT CCC GCT GAC AGT CAC AGT GGC -1

Met Ser Ala Leu Gly Ala Ala Pro Tyr Leu His His Pro Ala Asp Ser His Ser Gly 60

CGG GTC AGT TTC CTG GGT TCC CAG CCC TCT CCA GAA GTG ACG GCC GTG GCT CAG CTC TTG 120

Arg Val Ser Phe Leu Gly Ser Gln Pro Ser Pro Glu Val Thr Ala Val Ala Gln Leu Leu

AAG GAC TTA GAC AGG AGC ACC TTC AGA AAG TTG TTG AAA CTT GTA GTC GGG GCC CTG CAT 180

Lys Asp Leu Asp Arg Ser Thr Phe Arg Lys Leu Leu Lys Leu Val Val Gly Ala Leu His

GGG AAA GAC TGC AGA GAA GCT GTG GAG CAA CTT GGT GCC AGC GCC AAC CTG TCA GAA GAG 240

Gly Lys Asp Cys Arg Glu Ala Val Glu Gln Leu Gly Ala Ser Ala Asn Leu Ser Glu Glu

CGT CTG GCC GTC CTG CTG GCG GGC ACA CAC ACC CTG CTC CAG CAG GCT CTC CGG CTG CCC 300

Arg Leu Ala Val Leu Leu Ala Gly Thr His Thr Leu Leu Gln Gln Ala Leu Arg Leu Pro

CCT GCT AGT CTA AAG CCA GAT GCC TTC CAG GAA GAG CTC CAG GAA CTT GGC ATT CCT CAG 360

Pro Ala Ser Leu Lys Pro Asp Ala Phe Gln Glu Glu Leu Gln Glu Leu Gly Ile Pro Gln

GAT CTA ATT GGA GAT TTG GCC AGT TTG GCA TTT GGG AGT CAA CGC CCT CTT CTC GAC TCT 420

Asp Leu Ile Gly Asp Leu Ala Ser Leu Ala Phe Gly Ser Gln Arg Pro Leu Leu Asp Ser

GTA GCC CAA CAG CAG GGA TCC TCG CTG CCT CAC GTG TCT TAC TTC CGG TGG CGG GTG GAC 480

Val Ala Gln Gln Gln Gly Ser Ser Leu Pro His Val Ser Tyr Phe Arg Trp Arg Val Asp

GTG GCC ATC TCA ACC AGC GCT CAG TCC CGC TCC CTG CAA CCG AGT GTT CTC ATG CAG CTG 540

Val Ala Ile Ser Thr Ser Ala Gln Ser Arg Ser Leu Gln Pro Ser Val Leu Met Gln Leu

AAG CTC ACA GAT GGA TCT GCA CAC CGC TTC GAG GTG CCC ATA GCC AAA TTT CAG GAG CTG 600

Lys Leu Thr Asp Gly Ser Ala His Arg Phe Glu Val Pro Ile Ala Lys Phe Gln Glu Leu

CGG TAC AGT GTA GCC TTG GTC CTT AAG GAG ATG GCA GAA CTG GAG AAG AAG TGT GAG CGC 660

Arg Tyr Ser Val Ala Leu Val Leu Lys Glu Met Ala Glu Leu Glu Lys Lys Cys Glu Arg

AAA CTG CAG GAC TGA CTGAACCCCTGGTACTGTGGGTGCTGAAGCTGGTACCAGAACACAGCCCCCACTGGTGA 734

Lys Leu Gln Asp TER

TGAGCCCAACTCCATTGAGGTCTGTCATGTGAGAACGTATTTAAGTGAAAAGACAGCGGGACTTTTCAGGTTTTGTTTT 813

ATGAGTCAACAGCTGGGCAGGGTGGCACAGTTTATAATCTCAGCCCTTGAAGTCTGAGGCTGGAGAATGGGAAGTGTA 892

AGCTGGCCCTGGCTTTCATAGTGAGGCTCAGTGTGCGAATTAAAGAGGTAAAGCAACTATTAATAAAAAAAAAAAAAA 969

FIGURE 1

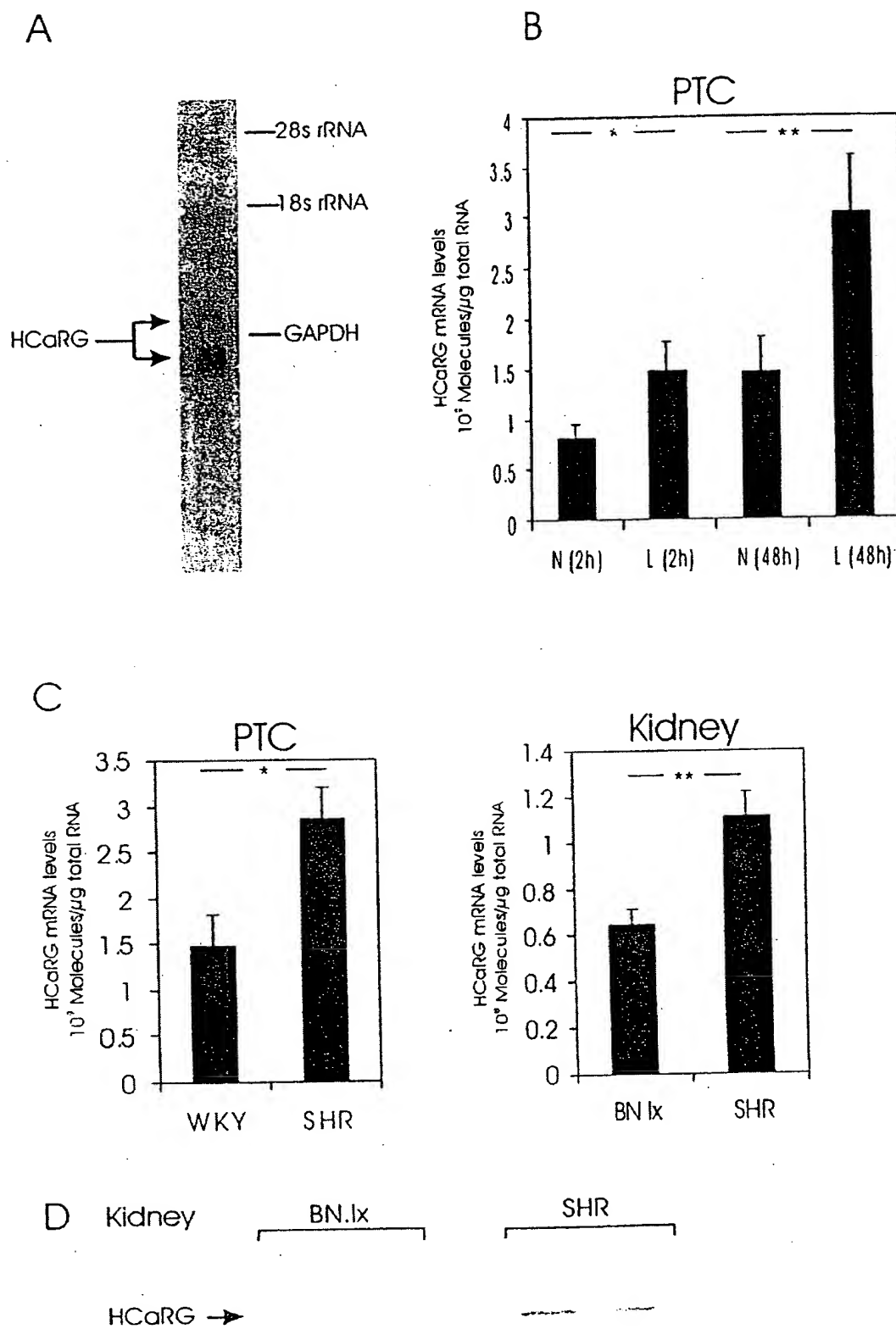


FIGURE 2

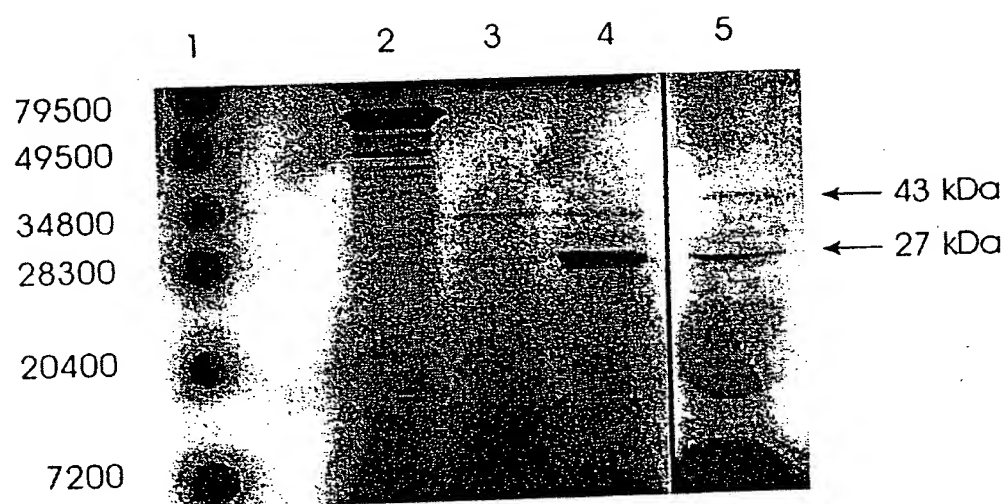


FIGURE 3

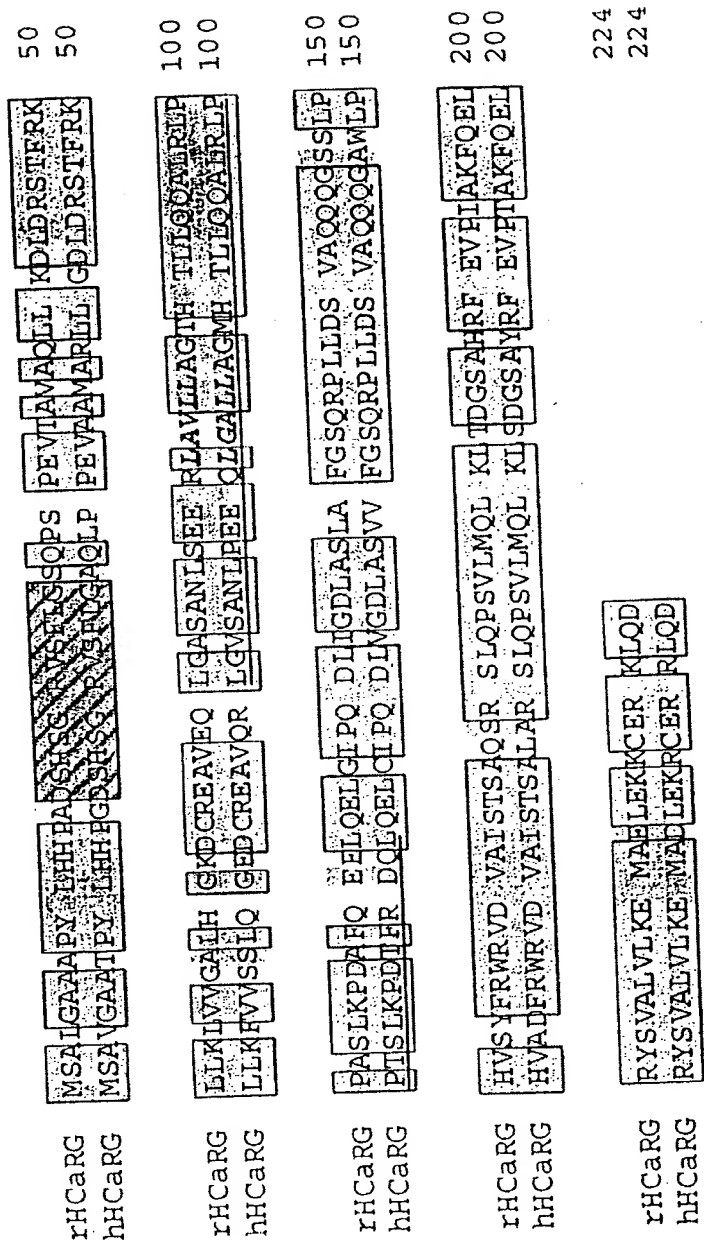
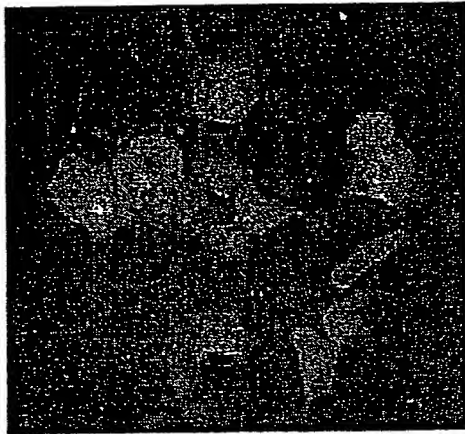
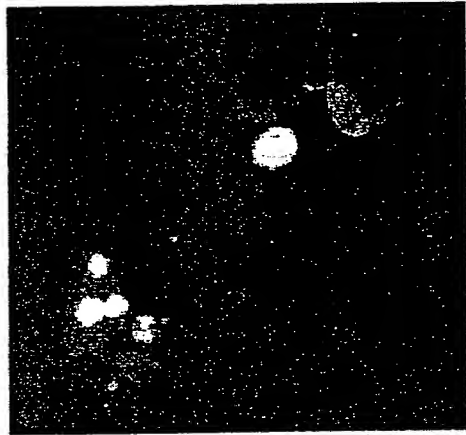


FIGURE 4

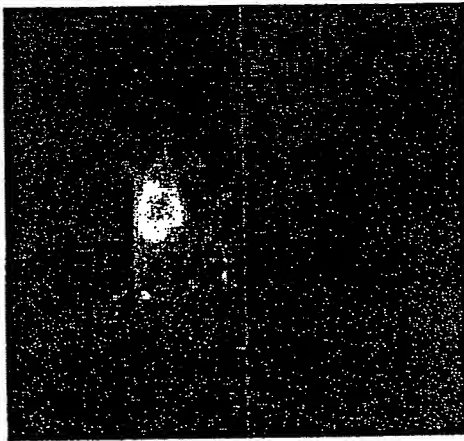
A



B



C



D

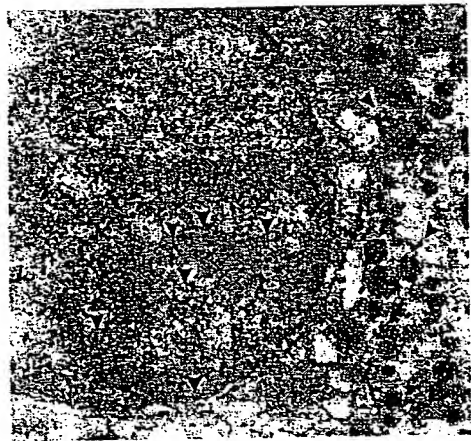


FIGURE 5

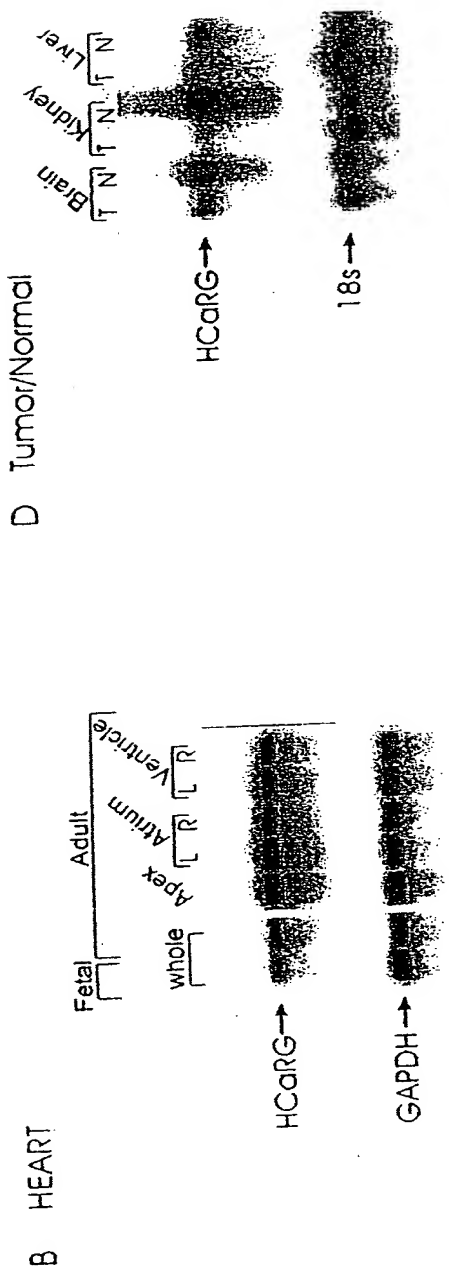
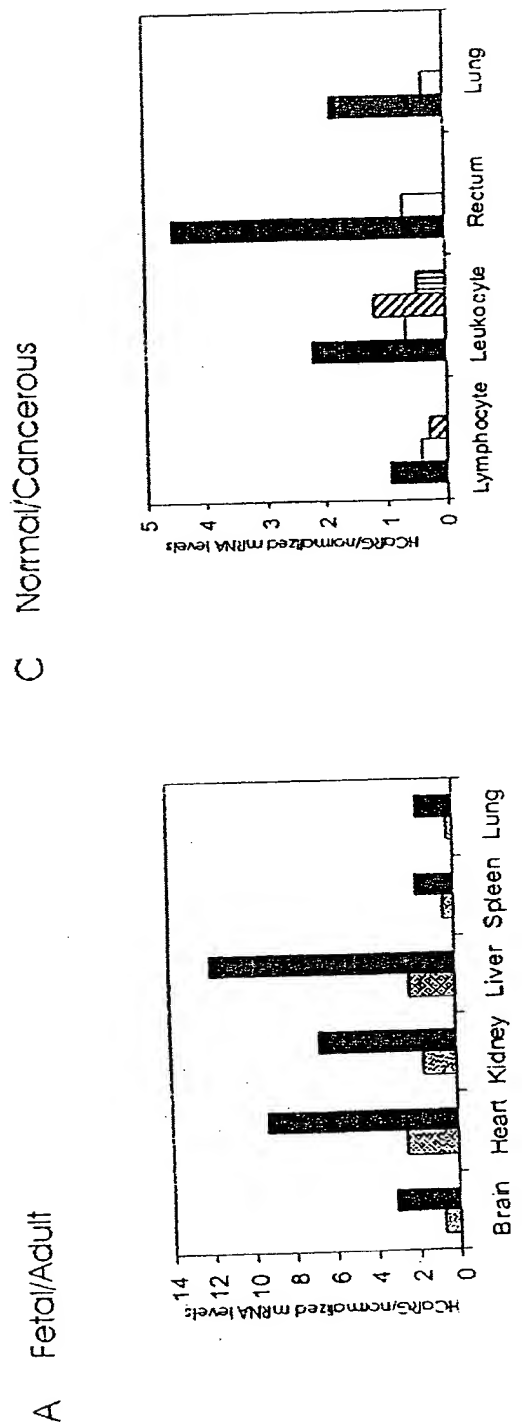


FIGURE 6

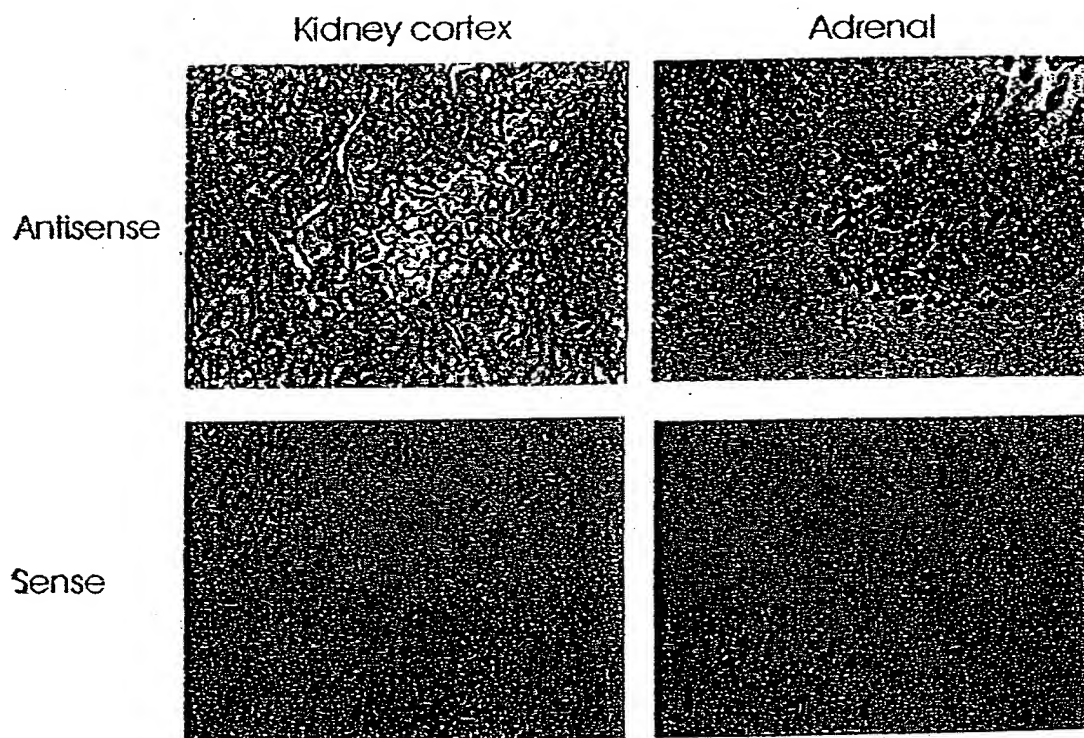
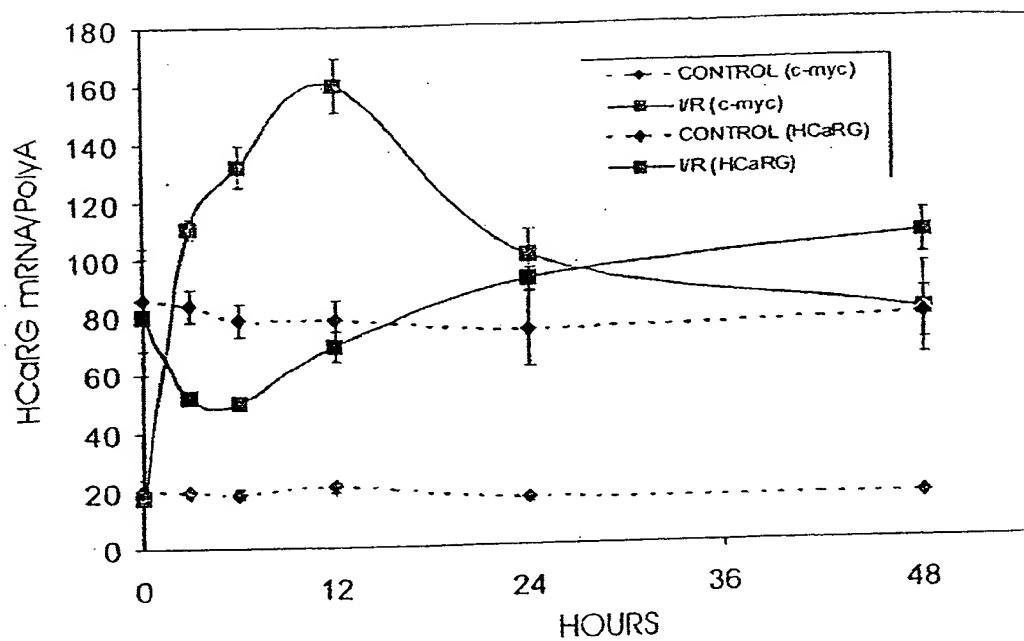
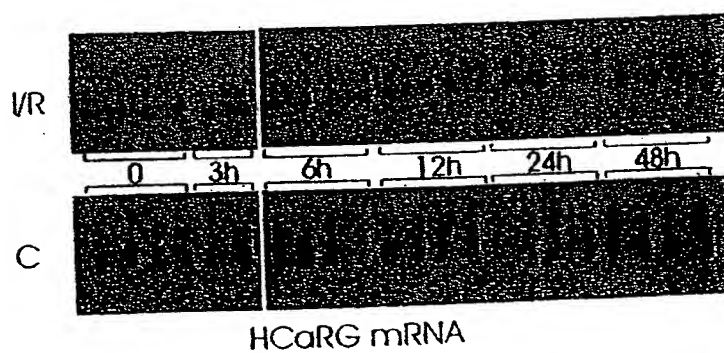


FIGURE 7

A Medulla



B Cortex



C Cortex

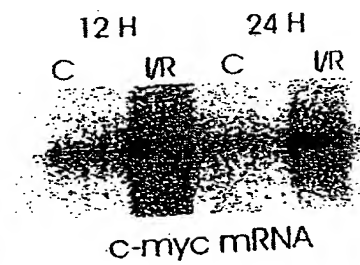
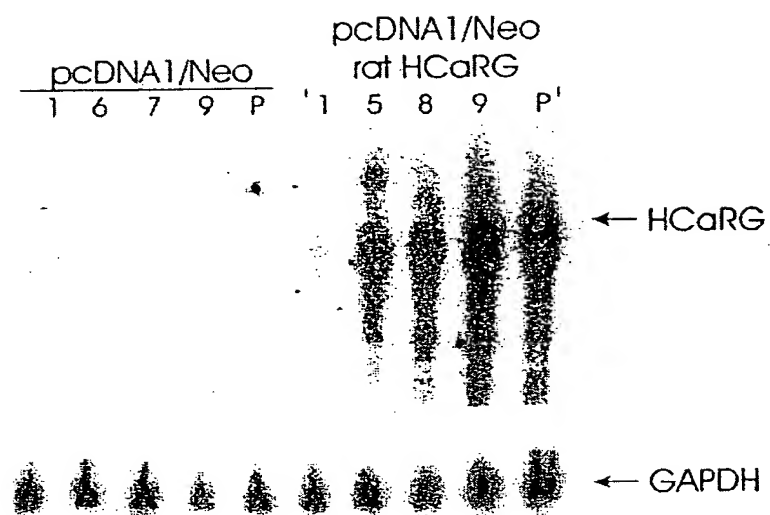


FIGURE 8

A



B

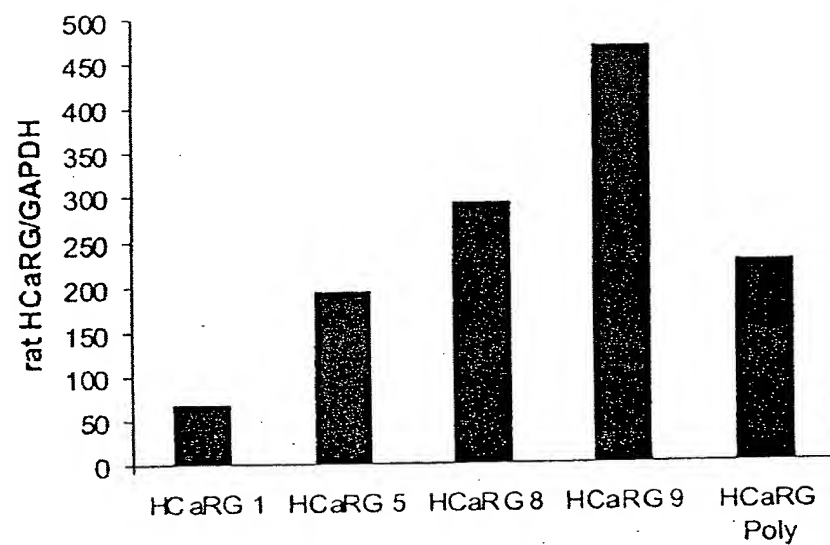
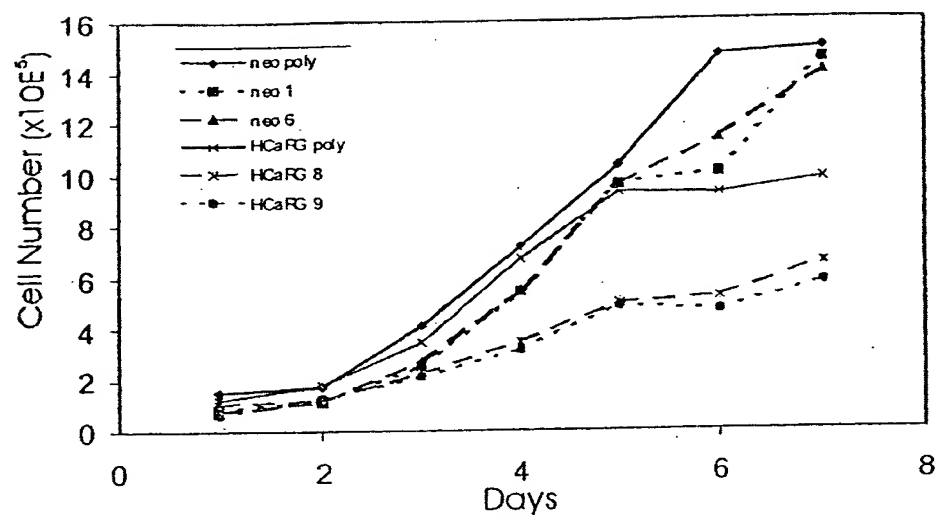


FIGURE 9

A



B

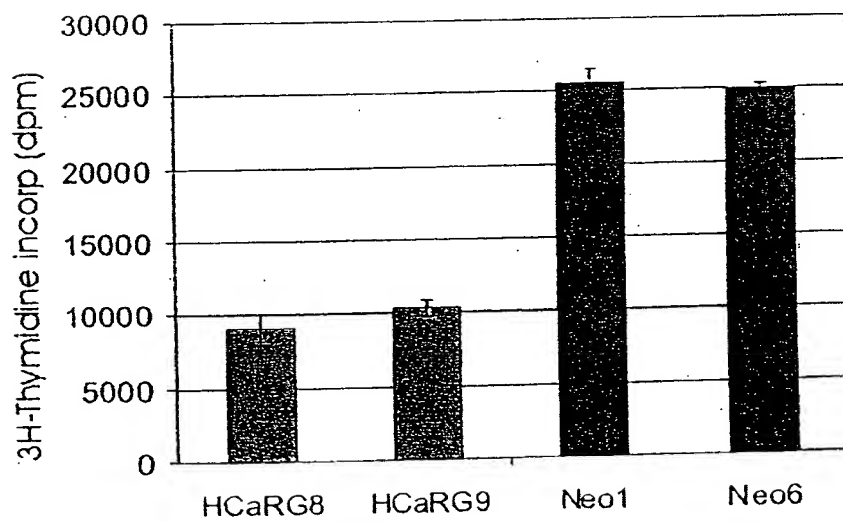
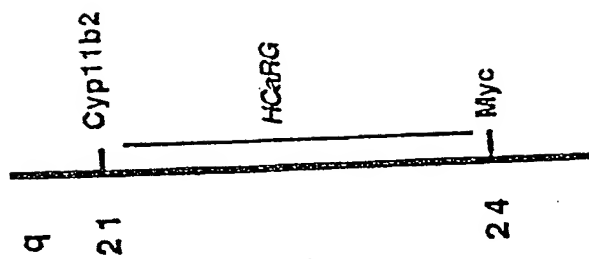
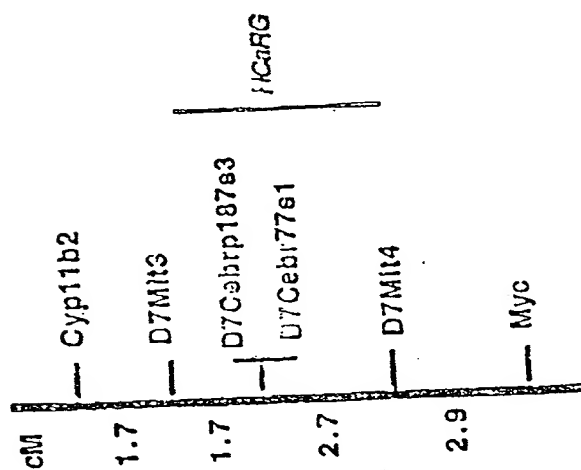


FIGURE 10

Human Chromosome 8



Rat Chromosome 7



Bgl II digestion

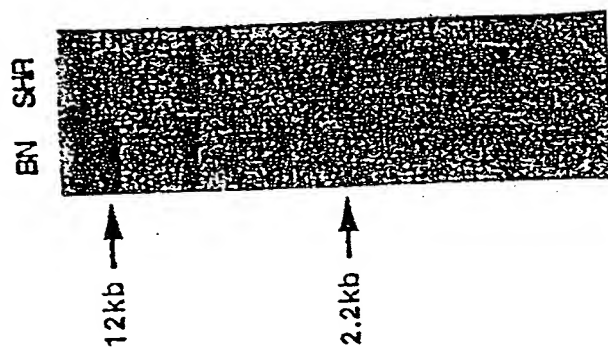


FIGURE 11